

# CRF Errors Corrected by the STIC Sys ms Branch

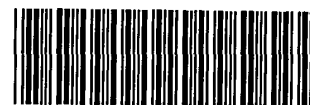
Serial Number: 09/995,804A

CRF Processing Dat : 4/3/02 # 6  
 Edited by: DC  
 Verified by: DC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: ENTERED
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING                      DATE: 04/03/2002  
 PATENT APPLICATION: US/09/995,804A      TIME: 11:40:52

Input Set : A:\PTO.DC.txt  
 Output Set: N:\CRF3\04032002\I995804A.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
 6     (i) APPLICANT: Engler, Jeffrey A  
 7                      Lee, Jae Hwy  
 8                      Collawan, James F  
 9                      Moore, Bryan A  
 11    (ii) TITLE OF INVENTION: Receptor-Mediated Uptake of Peptides  
 12                                      that Bind the Human Transferrin Receptor  
 14    (iii) NUMBER OF SEQUENCES: 13  
 16    (iv) CORRESPONDENCE ADDRESS:  
 17            (A) ADDRESSEE: Hendricks and Assoc.  
 18            (B) STREET: P.O. Box 2509  
 19            (C) CITY: Fairfax  
 20            (D) STATE: VA  
 21            (E) COUNTRY: U.S.A  
 22            (F) ZIP: 22031  
 24    (v) COMPUTER READABLE FORM:  
 25            (A) MEDIUM TYPE: Floppy disk  
 26            (B) COMPUTER: IBM PC compatible  
 27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 28            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 30    (vi) CURRENT APPLICATION DATA:  
 C--> 31            (A) APPLICATION NUMBER: US/09/995,804A  
 C--> 32            (B) FILING DATE: 29-Nov-2001  
 33            (C) CLASSIFICATION:  
 35    (viii) ATTORNEY/AGENT INFORMATION:  
 36            (A) NAME: Hendricks, Glenna M  
 37            (B) REGISTRATION NUMBER: 32,535  
 38            (C) REFERENCE/DOCKET NUMBER: engler1  
 40    (ix) TELECOMMUNICATION INFORMATION:  
 41            (A) TELEPHONE: 703/425-8405  
 42            (B) TELEFAX: 703/425-8406  
 45 (2) INFORMATION FOR SEQ ID NO: 1:  
 47    (i) SEQUENCE CHARACTERISTICS:  
 48            (A) LENGTH: 7 amino acids  
 49            (B) TYPE: amino acid  
 50            (C) STRANDEDNESS: single  
 51            (D) TOPOLOGY: unknown  
 53    (ii) MOLECULE TYPE: peptide  
 55    (iii) HYPOTHETICAL: NO  
 57    (iv) ANTI-SENSE: NO  
 61    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 63        His Ala Ile Tyr Pro Arg His

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64      1          5
66 (2) INFORMATION FOR SEQ ID NO: 2:
68      (i) SEQUENCE CHARACTERISTICS:
69          (A) LENGTH: 12 amino acids
70          (B) TYPE: amino acid
71          (C) STRANDEDNESS: single
72          (D) TOPOLOGY: unknown
74      (ii) MOLECULE TYPE: peptide
76      (iii) HYPOTHETICAL: NO
78      (iv) ANTI-SENSE: NO
82      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
84      Thr His Arg Pro Pro Met Trp Ser Pro Val Trp Pro
85      1          5          10
87 (2) INFORMATION FOR SEQ ID NO: 3:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 7 amino acids
91          (B) TYPE: amino acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: unknown
95      (ii) MOLECULE TYPE: peptide
97      (iii) HYPOTHETICAL: NO
99      (iv) ANTI-SENSE: NO
103     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
105     Ile Arg His Pro His Tyr Ala
106     1          5
108 (2) INFORMATION FOR SEQ ID NO: 4:
110     (i) SEQUENCE CHARACTERISTICS:
111         (A) LENGTH: 12 amino acids
112         (B) TYPE: amino acid
113         (C) STRANDEDNESS: single
114         (D) TOPOLOGY: unknown
116     (ii) MOLECULE TYPE: peptide
118     (iii) HYPOTHETICAL: NO
120     (iv) ANTI-SENSE: NO
124     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
126     Pro Trp Arg Pro Ser His Pro Val Trp Met Pro Thr
127     1          5          10
129 (2) INFORMATION FOR SEQ ID NO: 5:
131     (i) SEQUENCE CHARACTERISTICS:
132         (A) LENGTH: 18 base pairs
133         (B) TYPE: nucleic acid
134         (C) STRANDEDNESS: single
135         (D) TOPOLOGY: unknown
137     (ii) MOLECULE TYPE: DNA (genomic)
139     (iii) HYPOTHETICAL: NO
141     (iv) ANTI-SENSE: NO
145     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
147     TGGGATTTTG CTAAAAAC
149 (2) INFORMATION FOR SEQ ID NO: 6:

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## RAW SEQUENCE LISTING

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151      (i) SEQUENCE CHARACTERISTICS:
152          (A) LENGTH: 22 base pairs
153          (B) TYPE: nucleic acid
154          (C) STRANDEDNESS: single
155          (D) TOPOLOGY: unknown
157      (ii) MOLECULE TYPE: DNA (genomic)
159      (iii) HYPOTHETICAL: NO
161      (iv) ANTI-SENSE: NO
165      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
167 GTATGGGATT TTGCTAAACA AC                22
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 28 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: unknown
177      (ii) MOLECULE TYPE: DNA (genomic)
179      (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
187 TCTAGATCTG ATGAGTAAAG GAGAAGAA          28
189 (2) INFORMATION FOR SEQ ID NO: 8:
191      (i) SEQUENCE CHARACTERISTICS:
192          (A) LENGTH: 54 base pairs
193          (B) TYPE: nucleic acid
194          (C) STRANDEDNESS: single
195          (D) TOPOLOGY: unknown
197      (ii) MOLECULE TYPE: DNA (genomic)
199      (iii) HYPOTHETICAL: NO
201      (iv) ANTI-SENSE: NO
205      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
207 TTAAAGCTTT TAATGGCGCG GATAGATCGC ATGTTTGTAG AGCTCATCCA TGCC    54
209 (2) INFORMATION FOR SEQ ID NO: 9:
211      (i) SEQUENCE CHARACTERISTICS:
212          (A) LENGTH: 68 base pairs
213          (B) TYPE: nucleic acid
214          (C) STRANDEDNESS: single
215          (D) TOPOLOGY: unknown
217      (ii) MOLECULE TYPE: DNA (genomic)
219      (iii) HYPOTHETICAL: NO
221      (iv) ANTI-SENSE: NO
225      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
227 TAAAGCTTTT ACGGCCACAC CGGGCTCCAC ATCGGCGGGC GGTGGGTTTT GTAGAGCTCA 60
229 TCCATGCC                                68
231 (2) INFORMATION FOR SEQ ID NO: 10:
233      (i) SEQUENCE CHARACTERISTICS:
234          (A) LENGTH: 29 base pairs
235          (B) TYPE: nucleic acid
236          (C) STRANDEDNESS: single

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237      (D) TOPOLOGY: unknown
239      (ii) MOLECULE TYPE: DNA (genomic)
241      (iii) HYPOTHETICAL: NO
243      (iv) ANTI-SENSE: NO
247      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
249 GATCCCATGC GATCTATCCG CGCCATTAA                29
251 (2) INFORMATION FOR SEQ ID NO: 11:
253      (i) SEQUENCE CHARACTERISTICS:
254          (A) LENGTH: 29 base pairs
255          (B) TYPE: nucleic acid
256          (C) STRANDEDNESS: single
257          (D) TOPOLOGY: unknown
259      (ii) MOLECULE TYPE: DNA (genomic)
261      (iii) HYPOTHETICAL: NO
263      (iv) ANTI-SENSE: YES
267      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
269 GATCTTAATG GCGCGGATAG ATCGCATGG                29
271 (2) INFORMATION FOR SEQ ID NO: 12:
273      (i) SEQUENCE CHARACTERISTICS:
274          (A) LENGTH: 44 base pairs
275          (B) TYPE: nucleic acid
276          (C) STRANDEDNESS: single
277          (D) TOPOLOGY: unknown
279      (ii) MOLECULE TYPE: DNA (genomic)
281      (iii) HYPOTHETICAL: NO
283      (iv) ANTI-SENSE: NO
287      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
289 GATCCACCCA CCGCCCGCCG ATGTGGAGCC CGGTGTGGCC GTAA    44
291 (2) INFORMATION FOR SEQ ID NO: 13:
293      (i) SEQUENCE CHARACTERISTICS:
294          (A) LENGTH: 44 base pairs
295          (B) TYPE: nucleic acid
296          (C) STRANDEDNESS: single
297          (D) TOPOLOGY: unknown
299      (ii) MOLECULE TYPE: DNA (genomic)
301      (iii) HYPOTHETICAL: NO
303      (iv) ANTI-SENSE: YES
307      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
309 GATCTTACGG CCACACGGG CTCCACATCG GCGGGCGGTG GGTG    44

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VERIFICATION SUMMARY

DATE: 04/03/2002

PATENT APPLICATION: US/09/995,804A

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]